



SEQUENCE LISTING

<110> Lawton, Robert  
Mermer, Brion  
Francoeur, Greg

<120> Specific Binding Protein for Treating  
Canine Allergy

<130> 01-1275A

<140> 09/281,760

<141> 1999-03-30

<150> 09/058,331

<151> 1998-04-09

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Thr Leu Leu Glu Tyr Arg Met  
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Gly Met Asn Leu Thr Trp Tyr Arg Glu Ser Lys  
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<400> 8  
 Ser Ala Cys Pro Asn Pro His Asn Pro Tyr Cys Gly Gly Gly  
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 Val Thr Leu Cys Pro Asn Pro His Ile Pro Met Cys  
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Lys

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Val Asn Leu Thr Trp Ser Arg  
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Gly Met Thr Leu Thr Trp Ser Arg Glu Asn Gly  
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Gly Met Asn Leu Thr Trp Ser Arg Glu Ser Lys  
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Cys His Pro His Leu Pro Lys Arg Cys  
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Tyr Cys Arg Val Thr His Pro His Leu Pro Lys Asp Ile Val Arg Ser  
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Ile

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<211> 17

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Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala Leu Met Arg Ser  
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Thr

<210> 28

<211> 17

<212> PRT

<213> Cercopithecus aethiops

<400> 28

Gln Cys Arg Val Thr His Pro His Leu Pro Arg Ala Leu Val Arg Ser  
1 5 10 15  
Thr

<210> 29

<211> 17

<212> PRT

<213> Felis catus

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Gln Cys Lys Val Thr His Pro Asp Leu Pro Leu Val Ile Val Arg Ser  
1 5 10 15  
Ile

<210> 30

<211> 17

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<213> Sus scrofa

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Tyr Cys Asn Val Thr His Pro Asp Leu Pro Lys Pro Ile Leu Arg Ser



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aggcactgac actggncctg tccccacagc caccagccag gacctg tct gtg ttc 175  
Ser Val Phe  
1

ccc ttg gcc tcc tgc tgt aaa gac aac atc gcc agt acc tct gtt aca 223  
Pro Leu Ala Ser Cys Cys Lys Asp Asn Ile Ala Ser Thr Ser Val Thr  
5 10 15

ctg ggc tgt ctg gtc acc ggc tat ctc ccc atg tcg aca act gtg acc 271  
Leu Gly Cys Leu Val Thr Gly Tyr Leu Pro Met Ser Thr Thr Val Thr  
20 25 30 35

tgg gac acg ggg tct cta aat aag aat gtc acg acc ttc ccc acc acc 319  
Trp Asp Thr Gly Ser Leu Asn Lys Asn Val Thr Thr Phe Pro Thr Thr  
40 45 50

6 ttc cac gag acc tac ggc ctc cac agc atc gtc agc cag gtg acc gcc 367  
Phe His Glu Thr Tyr Gly Leu His Ser Ile Val Ser Gln Val Thr Ala  
55 60 65

tcg ggc gag tgg gcc aaa cag agg ttc acc tgc agc gtg gct cac nnt 415  
Ser Gly Glu Trp Ala Lys Gln Arg Phe Thr Cys Ser Val Ala His Xaa  
70 75 80

gag tcc acc gcc atc aac aag acc ttc agt gct aanccagggt tnnntggcca 468  
Glu Ser Thr Ala Ile Asn Lys Thr Phe Ser Ala  
85 90

catgacactg gagggagaag ggacaggctg gngaatgcgc catggctggt aacgcccagc 528

anatgtgggg ctggggctga cacatgagtc cctgtgggctn agagacacca ctgccacatg 588

gctgcctcta cttctagca tgt gcc tta aac ttc att ccg cct acc gtg aag 640  
Cys Ala Leu Asn Phe Ile Pro Pro Thr Val Lys  
95 100 105

ctc ttc cac tcc tcc tgc aac ccc gtc ggt gat acc cac acc acc atc 688  
Leu Phe His Ser Ser Cys Asn Pro Val Gly Asp Thr His Thr Thr Ile  
110 115 120

cag ctc ctg tgc ctc atc tct ggc tac gtc cca ggt gac atg gag gtc 736  
Gln Leu Leu Cys Leu Ile Ser Gly Tyr Val Pro Gly Asp Met Glu Val  
125 130 135

atc tgg ctg gtg gat ggg caa aag gct aca aac ata ttc cca tac act 784  
Ile Trp Leu Val Asp Gly Gln Lys Ala Thr Asn Ile Phe Pro Tyr Thr  
140 145 150

gca ccc ggc aca aag gag ggc aac gtg acc tct acc cac agc gag ctc	832
Ala Pro Gly Thr Lys Glu Gly Asn Val Thr Ser Thr His Ser Glu Leu	
155 160 165	
aac atc acc cag ggn nng tgn gta tcc caa aaa acc tac acc tgc cag	880
Asn Ile Thr Gln Gly Xaa Xaa Val Ser Gln Lys Thr Tyr Thr Cys Gln	
170 175 180 185	
gtc acc tat caa ggc ttt acc ttt aaa gat gag gct cgc aag tgc tca	928
Val Thr Tyr Gln Gly Phe Thr Phe Lys Asp Glu Ala Arg Lys Cys Ser	
190 195 200	
gag atggcccccc tgtccccag aaaccagat gcgcgaggct cagagatgag	981
Glu	
ggccaaggca cgccctcatg cagcctctca cacactgcag ag tcc gac ccc cga	1035
Ser Asp Pro Arg	
205	
ggc gtg agc agc tac ctg agc cca ccc agc ccc ctt gac ctg tat gtc	1083
Gly Val Ser Ser Tyr Leu Ser Pro Pro Ser Pro Leu Asp Leu Tyr Val	
210 215 220	
cac aag gcg ccc aag atc acc tgc ctg gta gtg gac ctg gcc acc atg	1131
His Lys Ala Pro Lys Ile Thr Cys Leu Val Val Asp Leu Ala Thr Met	
225 230 235	
gaa ggc atg aac ctg acc tgg tac cgg gag agc aaa gaa ccc gtg aac	1179
Glu Gly Met Asn Leu Thr Trp Tyr Arg Glu Ser Lys Glu Pro Val Asn	
240 245 250	
ccg gtc cct ttg aac aag aag gat cac ttc aat ggg acg atc aca gtc	1227
Pro Val Pro Leu Asn Lys Lys Asp His Phe Asn Gly Thr Ile Thr Val	
255 260 265 270	
acg tct acc ctg cca gtg aac acc aat gac tgg atc gag ggc gag acc	1275
Thr Ser Thr Leu Pro Val Asn Thr Asn Asp Trp Ile Glu Gly Glu Thr	
275 280 285	
tac tat tgc agg gtg acc cac ccg cac ctg ccc aag gac atc gtg cgc	1323
Tyr Tyr Cys Arg Val Thr His Pro His Leu Pro Lys Asp Ile Val Arg	
290 295 300	
tcc att gcc aag gcc cct ggt gagccacggg cccaggggag gtgggcgggc	1374
Ser Ile Ala Lys Ala Pro Gly	
305	
ctcctgancc ggagcctggg ctgacccac acctatccac aggc aag cgt gcc ccc	1430
Lys Arg Ala Pro	
310	
ccg gat gtg tac ttg ttc ctg cca ccg gag gag gag cag ggg acc aag	1478
Pro Asp Val Tyr Leu Phe Leu Pro Pro Glu Glu Glu Gln Gly Thr Lys	
315 320 325	
gac aga gtc acc ctc acg tgc ctg atc cag aac ttc ttc ccc gag gac	1526

Asp Arg Val Thr Leu Thr Cys Leu Ile Gln Asn Phe Phe Pro Glu Asp	
330 335 340 345	
att tca gtg caa tgg ctg cga aac gac agc ccc atc cag aca gac cag	1574
Ile Ser Val Gln Trp Leu Arg Asn Asp Ser Pro Ile Gln Thr Asp Gln	
350 355 360	
tac acc acc acg ggg ccc cac aag gtc tcg ggc tcc agg cct gcc ttc	1622
Tyr Thr Thr Thr Gly Pro His Lys Val Ser Gly Ser Arg Pro Ala Phe	
365 370 375	
ttc atc ttc agt cgc ctg gtg gac tgg gag cag aaa aac aaa ttc acc	1670
Phe Ile Phe Ser Arg Leu Val Asp Trp Glu Gln Lys Asn Lys Phe Thr	
380 385 390	
tgc caa gtg gtg cat gag gcg ctg tcc ggc tct agg atc ctc cag aaa	1718
Cys Gln Val Val His Glu Ala Leu Ser Gly Ser Arg Ile Leu Gln Lys	
395 400 405	
tgg gtg tcc aaa acc ccc ggt aaa tgatgccac cctcctcccg ccgccacccc	1772
Trp Val Ser Lys Thr Pro Gly Lys	
410 415	
ccagggctcc acctgctggg gcaggggagg ggggctggca agaccctcca tctatccttn	1832
tcaataaaca	1842

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<223> "n" stands for any nucleic acid

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<222> (413)..(414)

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<222> (460)..(462)

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1 5 10 15

Ser Val Thr Leu Gly Cys Leu Val Thr Gly Tyr Leu Pro Met Ser Thr  
20 25 30

Thr Val Thr Trp Asp Thr Gly Ser Leu Asn Lys Asn Val Thr Thr Phe  
35 40 45

Pro Thr Thr Phe His Glu Thr Tyr Gly Leu His Ser Ile Val Ser Gln  
50 55 60

Val Thr Ala Ser Gly Glu Trp Ala Lys Gln Arg Phe Thr Cys Ser Val  
65 70 75 80

Ala His Xaa Glu Ser Thr Ala Ile Asn Lys Thr Phe Ser Ala

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<223> The 'Xaa' at location 81 stands for Lys, Arg, Thr, Met, Glu, Gly, Ala, Val, Gln, Pro, Leu, a stop codon, Trp, or Ser.

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<223> The 'Xaa' at location 82 stands for a stop codon, Trp, or Cys.

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<400> 35

Cys Ala Leu Asn Phe Ile Pro Pro Thr Val Lys Leu Phe His Ser Ser  
1 5 10 15

Cys Asn Pro Val Gly Asp Thr His Thr Thr Ile Gln Leu Leu Cys Leu  
20 25 30

Ile Ser Gly Tyr Val Pro Gly Asp Met Glu Val Ile Trp Leu Val Asp  
35 40 45

Gly Gln Lys Ala Thr Asn Ile Phe Pro Tyr Thr Ala Pro Gly Thr Lys  
50 55 60

Glu Gly Asn Val Thr Ser Thr His Ser Glu Leu Asn Ile Thr Gln Gly  
65 70 75 80

Xaa Xaa Val Ser Gln Lys Thr Tyr Thr Cys Gln Val Thr Tyr Gln Gly  
85 90 95

Phe Thr Phe Lys Asp Glu Ala Arg Lys Cys Ser Glu  
100 105

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Ser Asp Pro Arg Gly Val Ser Ser Tyr Leu Ser Pro Pro Ser Pro Leu  
1 5 10 15

Asp Leu Tyr Val His Lys Ala Pro Lys Ile Thr Cys Leu Val Val Asp  
20 25 30

Leu Ala Thr Met Glu Gly Met Asn Leu Thr Trp Tyr Arg Glu Ser Lys  
35 40 45

Glu Pro Val Asn Pro Val Pro Leu Asn Lys Lys Asp His Phe Asn Gly  
50 55 60

Thr Ile Thr Val Thr Ser Thr Leu Pro Val Asn Thr Asn Asp Trp Ile  
65 70 75 80

Glu Gly Glu Thr Tyr Tyr Cys Arg Val Thr His Pro His Leu Pro Lys  
85 90 95

Asp Ile Val Arg Ser Ile Ala Lys Ala Pro Gly  
100 105

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<223> "n" stands for any nucleic acid

<400> 37

Lys Arg Ala Pro Pro Asp Val Tyr Leu Phe Leu Pro Pro Glu Glu Glu  
1 5 10 15

Gln Gly Thr Lys Asp Arg Val Thr Leu Thr Cys Leu Ile Gln Asn Phe  
20 25 30

Phe Pro Glu Asp Ile Ser Val Gln Trp Leu Arg Asn Asp Ser Pro Ile  
35 40 45

Gln Thr Asp Gln Tyr Thr Thr Thr Gly Pro His Lys Val Ser Gly Ser  
50 55 60

Arg Pro Ala Phe Phe Ile Phe Ser Arg Leu Val Asp Trp Glu Gln Lys  
65 70 75 80

Asn Lys Phe Thr Cys Gln Val Val His Glu Ala Leu Ser Gly Ser Arg  
85 90 95

Ile Leu Gln Lys Trp Val Ser Lys Thr Pro Gly Lys  
100 105

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Glu Gly Met Asn Leu Thr Trp Tyr Arg Glu Ser Lys Glu Pro Val Asn  
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ccg gtc cct ttg aac aag aag gat cac ttc aat ggg acg atc aca gtc 96  
Pro Val Pro Leu Asn Lys Lys Asp His Phe Asn Gly Thr Ile Thr Val  
20 25 30  
  
acg tct acc ctg cca gtg aac acc aat gac tgg atc gag ggc gag acc 144  
Thr Ser Thr Leu Pro Val Asn Thr Asn Asp Trp Ile Glu Gly Glu Thr  
35 40 45  
  
tac tat tgc agg gtg acc cac ccg cac ctg ccc aag gac atc gtg cgc 192  
Tyr Tyr Cys Arg Val Thr His Pro His Leu Pro Lys Asp Ile Val Arg  
50 55 60  
  
tcc att gcc aag gcc cct ggt 213  
Ser Ile Ala Lys Ala Pro Gly  
65 70

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<213> Canis familiaris

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Pro Val Pro Leu Asn Lys Lys Asp His Phe Asn Gly Thr Ile Thr Val  
20 25 30  
  
Thr Ser Thr Leu Pro Val Asn Thr Asn Asp Trp Ile Glu Gly Glu Thr  
35 40 45  
  
Tyr Tyr Cys Arg Val Thr His Pro His Leu Pro Lys Asp Ile Val Arg  
50 55 60  
  
Ser Ile Ala Lys Ala Pro Gly  
65 70